

SEQUENCE LISTING

<110> UAB Research Foundation
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Briles, David E.
Watt, James M.

<120> COMPOSITION FOR REDUCING BACTERIAL
CARRIAGE AND CNS INVASION AND METHODS OF USING SAME

<130> 21085.0067P1

<150> 60/518,799

<151> 2003-11-10

<160> 17

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
Synthetic Construct

<400> 1

atttctgtaa cagctaccaa cga

23

<210> 2

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
Synthetic Construct

<400> 2

gaattccctg tcttttcaaa gtc

23

<210> 3

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
Synthetic Construct

<400> 3

ccgatacact ctcttcccga

20

<210> 4

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
Synthetic Construct

<400> 4

acagttggtg ctaaggagggc

20

<210> 5

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
Synthetic Construct

<400> 5

Val Trp Arg Leu Leu Ala Pro Pro Phe Ser Asn Arg Leu Leu Pro
1 5 10 15

<210> 6

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
Synthetic Construct

<400> 6

cgcggtacct catactgggt taggaaagtc gtcg

34

<210> 7

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
Synthetic Construct

<400> 7

ggaattccat atgccgacag cagaactacc taaaggc

37

<210> 8

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
Synthetic Construct

<400> 8

ggaattccat atgctggcaa atgaaactca actttcgggg g

41

<210> 9

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
Synthetic Construct

<400> 9

cgcggatcca tcggctttga ccatcggag

29

<210> 10

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
Synthetic Construct

<400> 10

ggaattccat atgcgtattc cagcacttct caagacag

38

<210> 11

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
Synthetic Construct

<400> 11

ggaacattac ctcgcaaaag g

21

<210> 12

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
Synthetic Construct

<400> 12

tacccgcagg cataacatc

19

<210> 13

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
Synthetic Construct

<400> 13

Leu Pro Glu Thr Gly

1

5

<210> 14

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
Synthetic Construct

<221> VARIANT

<222> 3

<223> Xaa = any amino acid.

<400> 14

Leu Pro Xaa Thr Gly
1 5

<210> 15

<211> 1035

<212> PRT

<213> *S. pneumoniae*

<400> 15

Met	Ser	Tyr	Phe	Arg	Asn	Arg	Asp	Ile	Asp	Ile	Glu	Arg	Asn	Ser	Met	1	5	10	15
Asn	Arg	Ser	Val	Gln	Glu	Arg	Lys	Cys	Arg	Tyr	Ser	Ile	Arg	Lys	Leu	20	25	30	
Ser	Val	Gly	Ala	Val	Ser	Met	Ile	Val	Gly	Ala	Val	Val	Phe	Gly	Thr	35	40	45	
Ser	Pro	Val	Leu	Ala	Gln	Glu	Gly	Ala	Ser	Glu	Gln	Pro	Leu	Ala	Asn	50	55	60	
Glu	Thr	Gln	Leu	Ser	Gly	Glu	Ser	Ser	Thr	Leu	Thr	Asp	Thr	Glu	Lys	65	70	75	80
Ser	Gln	Pro	Ser	Ser	Glu	Thr	Glu	Leu	Ser	Gly	Asn	Lys	Gln	Glu	Gln	85	90	95	
Glu	Arg	Lys	Asp	Lys	Gln	Glu	Glu	Lys	Ile	Pro	Arg	Asp	Tyr	Tyr	Ala	100	105	110	
Arg	Asp	Leu	Glu	Asn	Val	Glu	Thr	Val	Ile	Glu	Lys	Glu	Asp	Val	Glu	115	120	125	
Thr	Asn	Ala	Ser	Asn	Gly	Gln	Arg	Val	Asp	Leu	Ser	Ser	Glu	Leu	Asp	130	135	140	
Lys	Leu	Lys	Lys	Leu	Glu	Asn	Ala	Thr	Val	His	Met	Glu	Phe	Lys	Pro	145	150	155	160
Asp	Ala	Lys	Ala	Pro	Ala	Phe	Tyr	Asn	Leu	Phe	Ser	Val	Ser	Ser	Ala	165	170	175	
Thr	Lys	Lys	Asp	Glu	Tyr	Phe	Thr	Met	Ala	Val	Tyr	Asn	Asn	Thr	Ala	180	185	190	
Thr	Leu	Glu	Gly	Arg	Gly	Ser	Asp	Gly	Lys	Gln	Phe	Tyr	Asn	Asn	Tyr	195	200	205	
Asn	Asp	Ala	Pro	Leu	Lys	Val	Lys	Pro	Gly	Gln	Trp	Asn	Ser	Val	Thr	210	215	220	
Phe	Thr	Val	Glu	Lys	Pro	Thr	Ala	Glu	Leu	Pro	Lys	Gly	Arg	Val	Arg	225	230	235	240
Leu	Tyr	Val	Asn	Gly	Val	Leu	Ser	Arg	Thr	Ser	Leu	Arg	Ser	Gly	Asn	245	250	255	
Phe	Ile	Lys	Asp	Met	Pro	Asp	Val	Thr	His	Val	Gln	Ile	Gly	Ala	Thr	260	265	270	
Lys	Arg	Ala	Asn	Asn	Thr	Val	Trp	Gly	Ser	Asn	Leu	Gln	Ile	Arg	Asn	275	280	285	
Leu	Thr	Val	Tyr	Asn	Arg	Ala	Leu	Thr	Pro	Glu	Glu	Val	Gln	Lys	Arg	290	295	300	
Ser	Gln	Leu	Phe	Lys	Arg	Ser	Asp	Leu	Glu	Lys	Lys	Leu	Pro	Glu	Gly	305	310	315	320

Ala Ala Leu Thr Glu Lys Thr Asp Ile Phe Glu Ser Gly Arg Asn Gly
 325 330 335
 Lys Pro Asn Lys Asp Gly Ile Lys Ser Tyr Arg Ile Pro Ala Leu Leu
 340 345 350
 Lys Thr Asp Lys Gly Thr Leu Ile Ala Gly Ala Asp Glu Arg Arg Leu
 355 360 365
 His Ser Ser Asp Trp Gly Asp Ile Gly Met Val Ile Arg Arg Ser Glu
 370 375 380
 Asp Asn Gly Lys Thr Trp Gly Asp Arg Val Thr Ile Thr Asn Leu Arg
 385 390 395 400
 Asp Asn Pro Lys Ala Ser Asp Pro Ser Ile Gly Ser Pro Val Asn Ile
 405 410 415
 Asp Met Val Leu Val Gln Asp Pro Glu Thr Lys Arg Ile Phe Ser Ile
 420 425 430
 Tyr Asp Met Phe Pro Glu Gly Lys Gly Ile Phe Gly Met Ser Ser Gln
 435 440 445
 Lys Glu Glu Ala Tyr Lys Lys Ile Asp Gly Lys Thr Tyr Gln Ile Leu
 450 455 460
 Tyr Arg Glu Gly Glu Lys Gly Ala Tyr Thr Ile Arg Glu Asn Gly Thr
 465 470 475 480
 Val Tyr Thr Pro Asp Gly Lys Ala Thr Asp Tyr Arg Val Val Val Asp
 485 490 495
 Pro Val Lys Pro Ala Tyr Ser Asp Lys Gly Asp Leu Tyr Lys Gly Asn
 500 505 510
 Gln Leu Leu Gly Asn Ile Tyr Phe Thr Thr Asn Lys Thr Ser Pro Phe
 515 520 525
 Arg Ile Ala Lys Asp Ser Tyr Leu Trp Met Ser Tyr Ser Asp Asp Asp
 530 535 540
 Gly Lys Thr Trp Ser Ala Pro Gln Asp Ile Thr Pro Met Val Lys Ala
 545 550 555 560
 Asp Trp Met Lys Phe Leu Gly Val Gly Pro Gly Thr Gly Ile Val Leu
 565 570 575
 Arg Asn Gly Pro His Lys Gly Arg Ile Leu Ile Pro Val Tyr Thr Thr
 580 585 590
 Asn Asn Val Ser His Leu Asn Gly Ser Gln Ser Ser Arg Ile Ile Tyr
 595 600 605
 Ser Asp Asp His Gly Lys Thr Trp His Ala Gly Glu Ala Val Asn Asp
 610 615 620
 Asn Arg Gln Val Asp Gly Gln Lys Ile His Ser Ser Thr Met Asn Asn
 625 630 635 640
 Arg Arg Ala Gln Asn Thr Glu Ser Thr Val Val Gln Leu Asn Asn Gly
 645 650 655
 Asp Val Lys Leu Phe Met Arg Gly Leu Thr Gly Asp Leu Gln Val Ala
 660 665 670
 Thr Ser Lys Asp Gly Gly Val Thr Trp Glu Lys Asp Ile Lys Arg Tyr
 675 680 685
 Pro Gln Val Lys Asp Val Tyr Val Gln Met Ser Ala Ile His Thr Met
 690 695 700
 His Glu Gly Lys Glu Tyr Ile Ile Leu Ser Asn Ala Gly Gly Pro Lys
 705 710 715 720
 Arg Glu Asn Gly Met Val His Leu Ala Arg Val Glu Glu Asn Gly Glu
 725 730 735
 Leu Thr Trp Leu Lys His Asn Pro Ile Gln Lys Gly Glu Phe Ala Tyr
 740 745 750
 Asn Ser Leu Gln Glu Leu Gly Asn Gly Glu Tyr Gly Ile Leu Tyr Glu
 755 760 765
 His Thr Glu Lys Gly Gln Asn Ala Tyr Thr Leu Ser Phe Arg Lys Phe
 770 775 780
 Asn Trp Asp Phe Leu Ser Lys Asp Leu Ile Ser Pro Thr Glu Ala Lys
 785 790 795 800

Val Lys Arg Thr Arg Glu Met Gly Lys Gly Val Ile Gly Leu Glu Phe
 805 810 815
 Asp Ser Glu Val Leu Val Asn Lys Ala Pro Thr Leu Gln Leu Ala Asn
 820 825 830
 Gly Lys Thr Ala Arg Phe Met Thr Gln Tyr Asp Thr Lys Thr Leu Leu
 835 840 845
 Phe Thr Val Asp Ser Glu Asp Met Gly Gln Lys Val Thr Gly Leu Ala
 850 855 860
 Glu Gly Ala Ile Glu Ser Met His Asn Leu Pro Val Ser Val Ala Gly
 865 870 875 890
 Thr Lys Leu Ser Asn Gly Met Asn Gly Ser Glu Ala Ala Val His Glu
 885 890 895
 Val Pro Glu Tyr Thr Gly Pro Leu Gly Thr Ser Gly Glu Glu Pro Ala
 900 905 910
 Pro Thr Val Glu Lys Pro Glu Tyr Thr Gly Pro Leu Gly Thr Ser Gly
 915 920 925
 Glu Glu Pro Ala Pro Thr Val Glu Lys Pro Glu Tyr Thr Gly Pro Leu
 930 935 940
 Gly Thr Ala Gly Glu Glu Ala Ala Pro Thr Val Glu Lys Pro Glu Phe
 945 950 955 960
 Thr Gly Gly Val Asn Gly Thr Glu Pro Ala Val His Glu Ile Ala Glu
 965 970 975
 Tyr Lys Gly Ser Asp Ser Leu Val Thr Leu Thr Thr Lys Glu Asp Tyr
 980 985 990
 Thr Tyr Lys Ala Pro Leu Ala Gln Gln Ala Leu Pro Glu Thr Gly Asn
 995 1000 1005
 Lys Glu Ser Asp Leu Leu Ala Ser Leu Gly Leu Thr Ala Phe Phe Leu
 1010 1015 1020
 Gly Leu Phe Thr Leu Gly Lys Lys Arg Glu Gln
 1025 1030 1035

<210> 16
 <211> 962
 <212> PRT
 <213> S. pneumoniae

<400> 16
 Met Asn Arg Ser Val Gln Glu Arg Lys Cys Arg Tyr Ser Ile Arg Lys
 1 5 10 15
 Leu Ser Val Gly Ala Val Ser Met Ile Val Gly Ala Val Val Asn Gly
 20 25 30
 Thr Ser Pro Val Leu Ala Gln Glu Gly Ala Ser Glu Gln Pro Leu Ala
 35 40 45
 Asn Glu Thr Gln Leu Ser Gly Glu Ser Ser Thr Leu Thr Asp Thr Glu
 50 55 60
 Lys Ser Gln Pro Ser Ser Glu Thr Glu Leu Ser Gly Asn Lys Gln Glu
 65 70 75 80
 Gln Glu Arg Lys Asp Lys Gln Glu Glu Lys Ile Pro Arg Asp Tyr Tyr
 85 90 95
 Ala Arg Asp Leu Glu Asn Val Glu Thr Val Ile Glu Lys Glu Asp Val
 100 105 110
 Glu Thr Asn Ala Ser Asn Gly Gln Arg Val Asp Leu Ser Ser Glu Leu
 115 120 125
 Asp Lys Leu Lys Lys Leu Glu Asn Ala Thr Val His Met Glu Asn Lys
 130 135 140
 Pro Asp Ala Lys Ala Pro Ala Phe Tyr Asn Leu Asn Ser Val Ser Ser
 145 150 155 160
 Ala Thr Lys Lys Asp Glu Tyr Phe Thr Met Ala Val Tyr Asn Asn Thr
 165 170 175

Ala Thr Leu Glu Gly Arg Gly Ser Asp Gly Lys Gln Asn Tyr Asn Asn
 180 185 190
 Tyr Asn Asp Ala Pro Leu Lys Val Lys Pro Gly Gln Trp Asn Ser Val
 195 200 205
 Thr Phe Thr Val Glu Lys Pro Thr Ala Glu Leu Pro Lys Gly Arg Val
 210 215 220
 Arg Leu Tyr Val Asn Gly Val Leu Ser Arg Thr Ser Leu Arg Ser Gly
 225 230 235 240
 Asn Phe Ile Lys Asp Met Pro Asp Val Thr His Val Gln Ile Gly Ala
 245 250 255
 Thr Lys Arg Ala Asn Asn Thr Val Trp Gly Ser Asn Leu Gln Ile Arg
 260 265 270
 Asn Leu Thr Val Tyr Asn Arg Ala Leu Thr Pro Glu Glu Val Gln Lys
 275 280 285
 Arg Ser Gln Leu Asn Lys Arg Ser Asp Leu Glu Lys Lys Leu Pro Glu
 290 295 300
 Gly Ala Ala Leu Thr Glu Lys Thr Asp Ile Phe Glu Ser Gly Arg Asn
 305 310 315 320
 Gly Asn Pro Asn Lys Asp Gly Ile Lys Ser Tyr Arg Ile Pro Ala Leu
 325 330 335
 Leu Lys Thr Asp Lys Gly Thr Leu Ile Ala Gly Ala Asp Glu Arg Arg
 340 345 350
 Leu His Ser Ser Asp Trp Gly Asp Ile Gly Met Val Ile Arg Arg Ser
 355 360 365
 Glu Asp Asn Gly Lys Thr Trp Gly Asp Arg Val Thr Ile Thr Asn Leu
 370 375 380
 Arg Asp Asn Pro Lys Ala Ser Asp Pro Ser Ile Gly Ser Pro Val Asn
 385 390 395 400
 Ile Asp Met Val Leu Val Gln Asp Pro Glu Thr Lys Arg Ile Asn Ser
 405 410 415
 Ile Tyr Asp Met Phe Pro Glu Gly Lys Gly Ile Asn Gly Met Ser Ser
 420 425 430
 Gln Lys Glu Glu Ala Tyr Lys Lys Ile Asp Gly Lys Thr Tyr Gln Ile
 435 440 445
 Leu Tyr Arg Glu Gly Glu Lys Gly Ala Tyr Thr Ile Arg Glu Asn Gly
 450 455 460
 Thr Val Tyr Thr Pro Asp Gly Lys Ala Thr Asp Tyr Arg Val Val Val
 465 470 475 480
 Asp Pro Val Lys Pro Ala Tyr Ser Asp Lys Gly Asp Leu Tyr Lys Gly
 485 490 495
 Asp Gln Leu Leu Gly Asn Ile Tyr Phe Thr Thr Asn Lys Thr Ser Pro
 500 505 510
 Asn Arg Ile Ala Lys Asp Ser Tyr Leu Trp Met Ser Tyr Ser Asp Asp
 515 520 525
 Asp Gly Lys Thr Trp Ser Ala Pro Gln Asp Ile Thr Pro Met Val Lys
 530 535 540
 Ala Asp Trp Met Lys Phe Leu Gly Val Gly Pro Gly Thr Gly Ile Val
 545 550 555 560
 Leu Arg Asn Gly Pro His Lys Gly Arg Ile Leu Ile Pro Val Tyr Thr
 565 570 575
 Thr Asn Asn Val Ser His Leu Asp Gly Ser Gln Ser Ser Arg Val Ile
 580 585 590
 Tyr Ser Asp Asp His Gly Lys Thr Trp His Ala Gly Glu Ala Val Asn
 595 600 605
 Asp Asn Arg Gln Val Asp Gly Gln Lys Ile His Ser Ser Thr Met Asn
 610 615 620
 Asn Arg Arg Ala Gln Asn Thr Glu Ser Thr Val Val Gln Leu Asn Asn
 625 630 635 640
 Gly Asp Val Lys Leu Asn Met Arg Gly Leu Thr Gly Asp Leu Gln Val
 645 650 655

Ala Thr Ser Lys Asp Gly Gly Val Thr Trp Glu Lys Asp Ile Lys Arg
 660 665 670
 Tyr Pro Gln Val Lys Asp Val Tyr Val Gln Met Ser Ala Ile His Thr
 675 680 685
 Met His Glu Gly Lys Glu Tyr Ile Ile Leu Ser Asn Ala Gly Gly Pro
 690 695 700
 Lys Arg Glu Asn Gly Met Val His Leu Ala Arg Val Glu Glu Asn Gly
 705 710 715 720
 Glu Leu Thr Trp Leu Lys His Asn Pro Ile Gln Lys Gly Glu Asn Ala
 725 730 735
 Tyr Asn Ser Leu Gln Glu Leu Gly Asn Gly Glu Tyr Gly Ile Leu Tyr
 740 745 750
 Glu His Thr Glu Lys Gly Gln Asn Ala Tyr Thr Leu Ser Asn Arg Lys
 755 760 765
 Asn Asn Trp Glu Asn Leu Ser Lys Asn Leu Ile Ser Pro Thr Glu Ala
 770 775 780
 Asn Asn Arg Asp Gly Gln Arg Arg Asp Gly Gln Arg Ser Tyr Trp Leu
 785 790 795 800
 Gly Val Arg Leu Arg Ser Ile Gly Gln Gln Gly Ser Asn Pro Ser Ile
 805 810 815
 Gly Lys Trp Asn Asn Ser Asp Asn Pro Asn Pro Val Asn Asn Gln Asp
 820 825 830
 Leu Val Val Cys Ser Arg Asn Gly Arg Tyr Arg Thr Gly Asn Tyr Trp
 835 840 845
 Tyr Ser Asn Arg Lys His Arg Lys Tyr Ala Asn Ser Ser Cys Lys Ser
 850 855 860
 Ser Arg Cys Gln Ser Ser Trp Arg Ser Lys Trp Asn Gln Ser Ser Gly
 865 870 875 880
 Ala Asn Ser Ser Arg Ile Tyr Arg Gly Ser Asn Trp Tyr Arg Ala Ser
 885 890 895
 Cys Ser Asn Asn Arg Arg Val Asn Gly Ile Asn Phe Ala Cys Asn Ser
 900 905 910
 Tyr Tyr Lys Lys Arg Leu Tyr Leu Gln Ser Ser Ser Cys Ser Ala Gly
 915 920 925
 Thr Ser Asn Asn Arg Lys Gln Gly Glu Asn Pro Pro Ser Phe Thr Arg
 930 935 940
 Thr Asn Ser Asn Leu Pro Trp Ser Val Tyr Ala Arg Glu Lys Glu Arg
 945 950 955 960
 Thr Ile

<210> 17

<211> 382

<212> PRT

<213> *S. typhimurium*

<400> 17

Met Thr Val Glu Lys Ser Val Val Phe Lys Ala Glu Gly Glu His Phe
 1 5 10 15
 Thr Asp Gln Lys Gly Asn Thr Ile Val Gly Ser Gly Ser Gly Thr
 20 25 30
 Thr Lys Tyr Phe Arg Ile Pro Ala Met Cys Thr Thr Ser Lys Gly Thr
 35 40 45
 Ile Val Val Phe Ala Asp Ala Arg His Asn Thr Ala Ser Asp Gln Ser
 50 55 60
 Phe Ile Asp Thr Ala Ala Arg Ser Thr Asp Gly Gly Lys Thr Trp
 65 70 75 80
 Asn Lys Lys Ile Ala Ile Tyr Asn Asp Arg Val Asn Ser Lys Leu Ser
 85 90 95
 Arg Val Met Asp Pro Thr Cys Ile Val Ala Asn Ile Gln Gly Arg Glu
 100 105 110
 Thr Ile Leu Val Met Val Gly Lys Trp Asn Asn Asn Asp Lys Thr Trp

		115					120					125				
Gly	Ala	Tyr	Arg	Asp	Lys	Ala	Pro	Asp	Thr	Asp	Trp	Asp	Leu	Val	Leu	
	130					135					140					
Tyr	Lys	Ser	Thr	Asp	Asp	Gly	Val	Thr	Phe	Ser	Lys	Val	Glu	Thr	Asn	
145					150					155					160	
Ile	His	Asp	Ile	Val	Thr	Lys	Asn	Gly	Thr	Ile	Ser	Ala	Met	Leu	Gly	
				165					170					175		
Gly	Val	Gly	Ser	Gly	Leu	Gln	Leu	Asn	Asp	Gly	Lys	Leu	Val	Phe	Pro	
			180					185					190			
Val	Gln	Met	Val	Arg	Thr	Lys	Asn	Ile	Thr	Thr	Val	Leu	Asn	Thr	Ser	
		195				200						205				
Phe	Ile	Tyr	Ser	Thr	Asp	Gly	Ile	Thr	Trp	Ser	Leu	Pro	Ser	Gly	Tyr	
	210					215					220					
Cys	Glu	Gly	Phe	Gly	Ser	Glu	Asn	Asn	Ile	Ile	Glu	Phe	Asn	Ala	Ser	
225					230					235					240	
Leu	Val	Asn	Asn	Ile	Arg	Asn	Ser	Gly	Leu	Arg	Arg	Ser	Phe	Glu	Thr	
				245					250					255		
Lys	Asp	Phe	Gly	Lys	Thr	Trp	Thr	Glu	Phe	Pro	Pro	Met	Asp	Lys	Lys	
			260					265					270			
Val	Asp	Asn	Arg	Asn	His	Gly	Val	Gln	Gly	Ser	Thr	Ile	Thr	Ile	Pro	
		275					280					285				
Ser	Gly	Asn	Lys	Leu	Val	Ala	Ala	His	Ser	Ser	Ala	Gln	Asn	Lys	Asn	
	290					295					300					
Asn	Asp	Tyr	Thr	Arg	Ser	Asp	Ile	Ser	Leu	Tyr	Ala	His	Asn	Leu	Tyr	
305					310					315					320	
Ser	Gly	Glu	Val	Lys	Leu	Ile	Asp	Asp	Phe	Tyr	Pro	Lys	Val	Gly	Asn	
				325					330					335		
Ala	Ser	Gly	Ala	Gly	Tyr	Ser	Cys	Leu	Ser	Tyr	Arg	Lys	Asn	Val	Asp	
			340					345					350			
Lys	Glu	Thr	Leu	Tyr	Val	Val	Tyr	Glu	Ala	Asn	Gly	Ser	Ile	Glu	Phe	
		355					360					365				
Gln	Asp	Leu	Ser	Arg	His	Leu	Pro	Val	Ile	Lys	Ser	Tyr	Asn			
	370					375					380					